CLAIMS

1. A method of inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain, comprising contacting said PDZ domain with an effective amount of an agent that competes with the binding of the C-terminal region of said cytoplasmic domain of MUC1 with said PDZ domain.

2. The method of claim 1, wherein said PDZ domain is ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751, MAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1.

3. The method of claim 1, wherein said agent that competes with binding of said C-terminal region of cytoplasmic domain of MUC1 with said PDZ domain is a peptide of the formula X^1-aa^2-aa^1-aa^0, wherein aa^0 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

4. The method of claim 3, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E .

5. The method of claim 3, wherein aa^2-aa^1-aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

6. The method of claim 3, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

7. The method of claim 3, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

8. The method of claim 3, wherein the amino terminus of X^1 comprises X^2-X^3, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

9. The method of claim 8, wherein X^2 is a sequence selected from SEQ ID NO 97 through SEQ ID NO: 127.

10. The method of claim 9, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.

11. A method of inhibiting the binding of the cytoplasmic domain of MUC1 to one or more PDZ proteins within a MUC1 expressing cancer cell comprising contacting said MUC1 expressing cancer cell with an effective amount of an agent that competes with the binding of the C-terminal region of said cytoplasmic domain of MUC1 with said PDZ protein.

12. The method of claim 11, wherein one or more PDZ proteins is/are selected from the group consisting of ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751, MAST2, and PRIL-16 d1.

13. The method of claim 11, wherein said agent that competes with binding of said C-terminal region of cytoplasmic domain of MUC1 with said one or more PDZ proteins is a peptide of the formula X^1-aa^2-aa^1-aa^0, wherein aa^0 is a hydrophobic aliphatic amino acid residue, aa^2 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

14. The method of claim 13, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E .

15. The method of claim 13, wherein aa^2-aa^1-aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

16. The method of claim 13, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

17. The method of claim 13, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

18. The method of claim 13, wherein the amino terminus of X^1 comprises X^2-X^3, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

19. The method of claim 18, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

20. The method of claim 19, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.

21. A method of enhancing the sensitivity of MUC1-expressing cancer cells to chemotherapeutic agents comprising contacting said MUC1-expressing cancer with an effective amount of a peptide of the formula X^1-aa^2-aa^1-aa^0, wherein aa^0 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

22. The method of claim 21, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E .

23. The method of claim 21, wherein aa^2-aa^1-aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

24. The method of claim 21, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

25. The method of claim 21, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

26. The method of claim 21, wherein the amino terminus of X^1 comprises X^2-X^3, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

27. The method of claim 26, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

28. The method of claim 27, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.

29. A method of killing MUC1-expressing cancer cells comprising contacting said MUC1-expressing cancer cells with an effective amount of a chemotherapeutic agent and an effective amount of a peptide of the formula X^1-aa^2-aa^1-aa^0, wherein aa^0 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

30. The method of claim 29, wherein said chemotherapeutic agent is a DNA-interactive agent, a tubulin interactive agent, and an antimetabolite chemotherapeutic agent.

31. The method of claim 29, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E .

32. The method of claim 29, wherein aa^2-aa^1-aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

33. The method of claim 29, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

34. The method of claim 29, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

35. The method of claim 29, wherein the amino terminus of X^1 comprises X^2-X^3, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

36. The method of claim 35, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

37. The method of claim 36, wherein X^2 is SEQ ID NO: 98, SEQ ID NO: 104 or SEQ ID NO: 119.

38. A method of killing MUC1-expressing cancer cells comprising contacting said MUC1-expressing cancer cells with an effective amount of a chemotherapeutic agent and an effective amount of an agent that inhibits the binding of the carboxy-terminal of the cytoplasmic tail of MUC1 with the PDZ domain of KIAA0751.

39. The method of claim 38, wherein said chemotherapeutic agent is a DNA-interactive agent, a tubulin interactive agent, and an antimetabolite chemotherapeutic agent.

40. The method of claim 38, wherein said agent that inhibits the binding of the carboxy-terminal of the cytoplamsic tail of MUC1 with the PDZ domain of KIAA0751 is a peptide of the formula X^1-aa^2-aa^1-aa^0, wherein aa^0 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

41. The method of claim 40, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E .

42. The method of claim 40, wherein aa^2-aa^1-aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

43. The method of claim 40, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

44. The method of claim 40, wherein the carboxy-terminus of said peptide of formula X^1-aa^2-aa^1-aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

45. The method of claim 40, wherein the amino terminus of X^1 comprises X^2-X^3, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

46. The method of claim 45, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

47. The method of claim 45, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.